

WHAT IS CLAIMED IS:

1. A cutinase variant comprising substituting one or more amino acids at residue positions corresponding to sites 57-66, 68, 85, 86, 88, 125-127, 130, 148-152, 154, 155, 176-183, or 204-211 of *Pseudomonas mendocina* cutinase SEQ ID NO: 2, and homologous cutinases thereof, and wherein said variant has polyesterase activity.
2. The cutinase of claim 1 derived from *Pseudomonas mendocina*.
3. The cutinase of claim 2, wherein the sequence is illustrated in SEQ ID NO: 2.
4. The cutinase of claim 1, wherein said variant includes the substitution of GLY 59 with one of Phe, Lys, Leu, Val enhances stability of the cutinase.
5. The cutinase of claim 1, wherein said variant includes the substitution of Thr 177 with one of His, Leu, Tyr enhances stability of the cutinase.
6. The cutinase of claim 1, wherein said variant includes the substitution of Thr 64 with one of Ala or Lle enhances stability of the cutinase.
7. The cutinase of claim 1, wherein said variant includes the substitution of Tyr 150 with Phe enhances stability of the cutinase.
8. The cutinase of claim 1, wherein said variant includes the substitution of Tyr 182 with one of Ala, Leu, or Pro enhances stability.
9. The cutinase of claim 1, wherein said variant includes the substitution of Phe 180 and substitution of Ser 205 enhances stability of the cutinase.
10. The cutinase of claim 1, wherein Phe is substituted with one of Ala, His, Lys, Leu, Asn, Pro or Glyc; and the Ser is substituted with Gly.
11. The cutinase of claim 1, wherein said variant includes the substitution of Ala 66 with Glx enhances polyesterase activity of the cutinase.
12. The cutinase of claim 1, wherein said variant includes the substitution of Phe 180 with one of Ala or His, and a substitution of Ser 205 with Gly enhances polyesterase activity of the cutinase.
13. The cutinase of claim 1, wherein said variant includes the substitution of Phe 180 with Ile enhances polyesterase activity of the cutinase.
14. The cutinase of claim 1, wherein said variant includes the substitution of Phe 180 with one of Lys or Leucine and substitution of Ser 205 with Gly enhances polyesterase activity of the cutinase.
15. The cutinase of claim 1, wherein said variant includes the substitution of Phy 180 with Asn enhances polyesterase activity of the cutinase.

16. The cutinase of claim 1, wherein said variant includes the substitution of Phe 180 with one of Asn, Pro, or Ser, and substitution of Ser 205 with Gly enhances polyesterase activity of the cutinase.
17. The cutinase of claim 1, wherein said variant includes the substitution of Gly 59 with Phe or Leucine enhances polyesterase activity of the cutinase.
18. The cutinase of claim 1, wherein said variant includes the substitution of Gly 61 with one of Asp or Glx enhances polyesterase activity of the cutinase.
19. The cutinase of claim 1, wherein said variant includes the following substitutions to enhance polyesterase activity of the cutinase: Ile 178 with Met; Phe 180 with Val; and Ser 205 with Gly.
20. The cutinase of claim 1, wherein said variant includes the substitution of Arg 20 with Gln and substitution of Tyr 112 enhance polyesterase activity of the cutinase.
21. The cutinase of claim 1, wherein said variant includes the substitution of Ser 205 with Asn and substitution of Phe 207 with Leu enhance polyesterase activity.
22. The cutinase of claim 1, wherein said variant includes the substitution of Ser 63 with Arg enhances polyesterase activity of the cutinase.
23. The cutinase of claim 1, wherein said variant includes the substitution of Ser 85 with Lys enhances polyesterase activity of the cutinase.
24. The cutinase of claim 1, wherein said variant includes the substitution of Thr 177 with one of His, Leu, or Tyr enhances polyesterase activity of the cutinase.
25. The cutinase of claim 1, wherein said variant includes the substitution of Thr 64 with Leu enhances polyesterase activity.
26. The cutinase of claim 1, wherein said variant includes the substitution of Tyr 182 with one of Ala or Pro enhances polyesterase activity.
27. The cutinase of claim 1, wherein said variant includes the substitution of Phe 180 with one of Ile, Leu, Asn, and Pro enhances stability of the cutinase.
28. A cutinase variant having one or more amino acid substitutions at residue positions corresponding to sites 57-66, 68, 85, 86, 88, 125-127, 130, 148-152, 154, 155, 176-183, or 204-211 of *Pseudomonas mendocina* cutinase SEQ ID NO: 2, and homologous cutinases thereof, wherein said variant is thermostable and has hydrolytic activity on polyester.
29. The cutinase variant of claim 28 derived from *Pseudomonas* species.